AMENDMENTS TO THE CLAIMS:

Please amend the claims as follows:

Claims 1-15. (Canceled)

16. (Previously Presented) The method according to claim 35, wherein the HBV genotype A specific target sequence in the HBsAg region is selected from the HBsAg region of the group consisting of SEQ ID NOs: 279-283.

Claim 17. (Canceled)

18. (Withdrawn) The method according to claim 35 or claim 16, characterized further by determining the presence or absence of HBV genotype B, wherein the probe(s) of step (iii) hybridize(s) specifically to a HBV genotype B specific target sequence in the HBsAg region.

19. (Withdrawn) The method according to claim 18, wherein the HBV genotype B specific target sequence is SEQ ID NO: 78, or the complement thereof.

20. (Withdrawn) The method according to claim 35 or claim 16, characterized further by determining the presence or absence of HBV genotype C, wherein the probe(s) of step (iii) hybridize(s) specifically to a HBV genotype C specific target sequence.

21. (Withdrawn) The method according to claims 20, wherein the HBV genotype C specific target sequence is selected from the group consisting of SEQ ID NO: 153, SEQ ID NO: 154 and SEQ ID NO: 204, or the complement thereof.

22. (Withdrawn) The method according to claim 35 or claim 16, characterized further by determining the presence or absence of HBV genotype D, wherein the

probe(s) of step (iii) hybridize(s) specifically to a HBV genotype D specific target sequence.

23. (Withdrawn) The method according to claim 22, wherein the HBV genotype D specific target is selected from the group consisting of SEQ ID NO: 165 and SEQ ID NO: 208, or the complement thereof.

24. (Withdrawn) The method according to claim 35 or claim 16, characterized further by determining the presence or absence of HBV genotype E, wherein the probe(s) of step (iii) hybridize(s) specifically to a HBV genotype E specific target sequence.

25. (Withdrawn) The method according to claim 24, wherein the HBV genotype E specific target sequence is selected from the group consisting of SEQ ID NO: 172 and SEQ ID NO: 213, or the complement thereof.

26. (Withdrawn) The method according to claim 35 or claim 16, characterized further by determining the presence or absence of HBV genotype F, wherein the probe(s) of step (iii) hybridize(s) specifically to a HBV genotype F specific target sequence.

27. (Withdrawn) The method according to claim 26, wherein the HBV genotype F specific target sequence is selected from the group consisting of SEQ ID NO: 186, SEQ ID NO: 216 and SEQ ID NO: 219, or the complement thereof.

28. (Currently Amended) The method according to claim 35 or claim 16 wherein the primer is selected from the group consisting of SEQ ID NOs: 75-76, 94, 104, 105, 112 and 134-135.

29. (Previously Presented) The method according to claim 35 or claim 16 wherein step (iii) is a reverse hybridization step.

Claim 30. (Canceled)

31. (Withdrawn) A probe specifically hybridizing to a HBV genotype A specific target sequence in the HBsAg region of HBV, said target sequence being selected from the group consisting of SEQ ID NO: 77, SEQ ID NO: 140, SEQ ID NO: 148 and SEQ ID NO: 193, or the complement thereof.

32. (Withdrawn) A composition comprising at least two probes specifically hybridizing to a HBV genotype specific target sequence in the HbsAg region of HBV, said target sequence for genotype A being selected from the group consisting of SEQ ID NO: 77, SEQ ID NO: 140, SEQ ID NO: 148 and SEQ ID NO: 193, or the complement thereof; for genotype B being selected from the group consisting of SEQ ID NO: 78 and SEQ ID NO: 148, or the complement thereof; for genotype C being selected from the group consisting of SEQ ID NO: 80, SEQ ID NO: 153, SEQ ID NO: 154 and SEQ ID NO: 204, or the complement thereof; for genotype D being selected from the group consisting of SEQ ID NO: 80, SEQ ID NO: 165 and SEQ ID NO: 208, or the complement thereof; for genotype E being selected from the group consisting of SEQ ID NO: 80, SEQ ID NO: 172, SEQ ID NO: 177 and SEQ ID NO: 213, or the complement thereof; for genotype F being selected from the group consisting of SEQ ID NO: 177, SEQ ID NO: 216, SEQ ID NO: 219 and SEQ ID NO: 186, or the complement thereof.

Claim 33. (Canceled)

34. (Withdrawn) An assay kit for diagnosing or monitoring HBV genotypes present in a biological sample comprising at least one of the probes according to claim 31, optionally fixed to a solid support.

35. (Currently Amended) A method for determining the presence or absence of HBV genotype A in a biological sample, comprising:

(i) providing a biological sample comprising polynucleic acids;

(ii) optionally releasing, isolating and/or concentrating the polynucleic acids present in the sample;

(iii) optionally amplifying the HBsAg region, or part thereof, of the HBV gene present in said sample with at least one ~~suitable~~ primer pair;

([[iii]]iv) hybridizing the polynucleic acids of step (i) or (ii) or (iii) with at least one nucleotide probe selected from the group consisting of a sequence of 5-17 nucleotides long of ~~which hybridizes specifically to~~ SEQ ID NO 77, a sequence of 5-19 nucleotides long of ~~which hybridizes specifically to~~ SEQ ID NO 140, and a sequence of 5-18 nucleotides long of ~~which hybridizes specifically to~~ SEQ ID NO 193;

([[i]]v) detecting the hybrid(s) formed in step ([[iii]]iv);

(vi) inferring the HBV genotype present in said sample from the hybridization signal(s) obtained in step ([[i]]v).

36. (Currently Amended) A method for determining the presence or absence of HBV genotype A in a biological sample, comprising:

(i) providing a biological sample comprising polynucleic acids;

(ii) optionally releasing, isolating and/or concentrating the polynucleic acids present in the sample;

(iii) ~~optionally~~ amplifying the HBsAg region, or part thereof, of the HBV gene present in said sample with at least one suitable primer pair, at least one primer of said primer pair being selected from the group consisting of SEQ ID NOs: 75[[-]], 76, 94, 104, 105, 112 and 134-135;

([[iii]]iv) hybridizing under stringent conditions the polynucleic acids of step (iii) ~~or (ii)~~ with at least one nucleotide probe of about 5 to 50 nucleotides long hybridizing specifically to a HBV genotype A specific target sequence in the HBsAg region of HBV selected from the HBsAg region of the group consisting of SEQ ID NOs: 279-283;

([[i]]v) detecting the hybrid(s) formed in step ([[iii]]iv);

(vi) inferring the HBV genotype present in said sample from the hybridization signal(s) obtained in step ([[i]]v).

37. (Previously Presented) The method according to claim 36, wherein the HBV genotype A specific target sequence is selected from the group consisting of SEQ ID NO: 77, SEQ ID NO: 140 and SEQ ID NO: 193, or the complement thereof.

Claim 38. (Canceled)

39. (Previously Presented) The method according to claim 36 wherein step (iii) is a reverse hybridization step.

40. (Previously Presented) The method according to claim 37 wherein step (iii) is a reverse hybridization step.